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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/087,167

DATE: 03/22/2002

TIME: 10:47:24

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\03222002\J087167.raw

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3 <110> APPLICANT: Pascal, Erica
4     Valentine, Scott
5     Brown, Jeffrey
6     Cockrell, Adam
7     Johnson, Brian
9 <120> TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
11 <130> FILE REFERENCE: 50018A
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/087,167
C--> 13 <141> CURRENT FILING DATE: 2002-03-01
13 <150> PRIOR APPLICATION NUMBER: US 60/242,969
14 <151> PRIOR FILING DATE: 2000-10-24
16 <160> NUMBER OF SEQ ID NOS: 148
18 <170> SOFTWARE: PatentIn version 3.1
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21 <211> LENGTH: 2840
22 <212> TYPE: DNA
23 <213> ORGANISM: Manduca sexta
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (361)..(2031)
28 <223> OTHER INFORMATION: Manduca sexta Ecdysone Receptor
31 <300> PUBLICATION INFORMATION:
32 <301> AUTHORS: Fujiwara, et al.
33 <302> TITLE: Cloning of an ecdysone receptor homolog from Manduca sexta and the
34     developmental profile of its mRNA in wings
35 <303> JOURNAL: Insect Biochem. Mol. Biol.
36 <304> VOLUME: 25
37 <305> ISSUE: 7
38 <306> PAGES: 845-856
39 <307> DATE: 1995
40 <308> DATABASE ACCESSION NO: Genbank/U19812
41 <309> DATABASE ENTRY DATE: 1996-02-03
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48 cttcggattg tgttgtgact gaaaagcgac gcgtatcggtg gtcgaagatt ctctataagt      180
50 gcataatata ttcgagacag tggatagcga ttctgtttcgg ttctatcgcg cggtatgagt      240
52 gttcatgccc gtagagacgc gtttagatag ttatggcgag gaaaaagtga agtgaaagcc      300
54 tacgtcagag gatgtccctc ggtgggtcacg gaagccgggg cgtgtgacgc gctcttcgac      360
56 atg aga cgc cgc tgg tca aac aac gga tgt ttc cct ctg cga atg ttt      408
57 Met Arg Arg Arg Trp Ser Asn Asn Gly Cys Phe Pro Leu Arg Met Phe
58 1          5          10          15
60 gag gag agc tcc tct gaa gtg act tct tcc tcg gcg ttc ggg atg ccg      456

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62				20					25					30			
64	gcg	gcc	atg	gta	atg	tca	ccg	gag	tcg	ctg	gcg	tcg	cca	gag	tac	ggc	504
65	Ala	Ala	Met	Val	Met	Ser	Pro	Glu	Ser	Leu	Ala	Ser	Pro	Glu	Tyr	Gly	
66			35					40					45				
68	ggc	ctc	gag	ctc	tgg	agc	tac	gat	gag	acc	atg	aca	aac	tat	ccg	gcg	552
69	Gly	Leu	Glu	Leu	Trp	Ser	Tyr	Asp	Glu	Thr	Met	Thr	Asn	Tyr	Pro	Ala	
70		50					55					60					
72	cag	tca	ctg	ctc	ggc	gcg	tgt	aat	gcg	ccg	cag	cag	cag	cag	caa	cag	600
73	Gln	Ser	Leu	Leu	Gly	Ala	Cys	Asn	Ala	Pro	Gln	Gln	Gln	Gln	Gln	Gln	
74	65					70				75					80		
76	caa	caa	cag	cag	ccg	tcc	gct	cag	ccg	ctg	ccg	tct	atg	ccg	ctg	ccg	648
77	Gln	Gln	Gln	Gln	Pro	Ser	Ala	Gln	Pro	Leu	Pro	Ser	Met	Pro	Leu	Pro	
78					85				90					95			
80	atg	cct	cct	aca	act	cct	aaa	tca	gag	aac	gag	tcc	atg	tcg	tca	ggc	696
81	Met	Pro	Pro	Thr	Thr	Pro	Lys	Ser	Glu	Asn	Glu	Ser	Met	Ser	Ser	Gly	
82				100					105					110			
84	cga	gaa	gaa	tta	tca	ccg	gcc	tca	agt	ata	aat	gga	tgt	agt	act	gat	744
85	Arg	Glu	Glu	Leu	Ser	Pro	Ala	Ser	Ser	Ile	Asn	Gly	Cys	Ser	Thr	Asp	
86			115					120					125				
88	ggg	gaa	cca	aga	cga	cag	aag	aaa	ggg	cca	gcg	ccg	cgc	cag	cag	gag	792
89	Gly	Glu	Pro	Arg	Arg	Gln	Lys	Lys	Gly	Pro	Ala	Pro	Arg	Gln	Gln	Glu	
90		130					135				140						
92	gaa	ctg	tgc	ctt	gtt	tgc	ggc	gac	agg	gct	tcg	gga	tat	cac	tat	aac	840
93	Glu	Leu	Cys	Leu	Val	Cys	Gly	Asp	Arg	Ala	Ser	Gly	Tyr	His	Tyr	Asn	
94	145					150				155					160		
96	gcg	ctt	acg	tgc	gaa	gga	tgt	aaa	ggg	ttc	ttc	agg	cgg	agt	gtg	acc	888
97	Ala	Leu	Thr	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	Ser	Val	Thr	
98				165					170					175			
100	aag	aat	gcg	gta	tat	att	tgt	aaa	ttt	gga	cac	gcc	tgc	gag	atg	gac	936
101	Lys	Asn	Ala	Val	Tyr	Ile	Cys	Lys	Phe	Gly	His	Ala	Cys	Glu	Met	Asp	
102				180					185					190			
104	atg	tac	atg	agg	aga	aaa	tgc	caa	gag	tgt	cgg	ttg	aag	aaa	tgc	ctc	984
105	Met	Tyr	Met	Arg	Arg	Lys	Cys	Gln	Glu	Cys	Arg	Leu	Lys	Lys	Cys	Leu	
106			195					200					205				
108	gcg	gtg	ggc	atg	agg	ccc	gag	tgc	gtc	gtc	cca	gag	tcc	acg	tgc	aag	1032
109	Ala	Val	Gly	Met	Arg	Pro	Glu	Cys	Val	Val	Pro	Glu	Ser	Thr	Cys	Lys	
110		210					215					220					
112	aac	aaa	aga	aga	gaa	aag	gaa	gca	cag	aga	gaa	aaa	gac	aaa	ctg	cca	1080
113	Asn	Lys	Arg	Arg	Glu	Lys	Glu	Ala	Gln	Arg	Glu	Lys	Asp	Lys	Leu	Pro	
114	225				230					235					240		
116	gtc	agt	acg	acg	aca	gtg	gac	gat	cat	atg	cct	gcc	ata	atg	caa	tgt	1128
117	Val	Ser	Thr	Thr	Thr	Val	Asp	Asp	His	Met	Pro	Ala	Ile	Met	Gln	Cys	
118				245					250					255			
120	gac	cct	ccg	ccc	cca	gag	gcg	gca	agg	att	cac	gaa	gtg	gtc	ccg	agg	1176
121	Asp	Pro	Pro	Pro	Pro	Glu	Ala	Ala	Arg	Ile	His	Glu	Val	Val	Pro	Arg	
122				260					265					270			
124	ttc	cta	acg	gag	aag	cta	atg	gag	cag	aac	aga	ctg	aag	aat	gtg	acg	1224
125	Phe	Leu	Thr	Glu	Lys	Leu	Met	Glu	Gln	Asn	Arg	Leu	Lys	Asn	Val	Thr	

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128 ccg ctg tcg gcg aac cag aag tcc ctg atc gcg agg ctc gtg tgg tac				1272
129 Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr				
130 290	295	300		
132 cag gag ggg tac gag cag ccg tcg gag gaa gat ctc aag aga gtt aca				1320
133 Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val Thr				
134 305	310	315	320	
136 cag aca tgg cag tta gaa gaa gaa gaa gag gag gaa act gac atg ccc				1368
137 Gln Thr Trp Gln Leu Glu Glu Glu Glu Glu Glu Glu Thr Asp Met Pro				
138 325	330	335		
140 ttc cgt cag atc aca gag atg acg atc tta aca gtg cag ctt att gta				1416
141 Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val				
142 340	345	350		
144 gaa ttc gca aag gga cta ccg gga ttc tcc aag ata tct cag tcc gat				1464
145 Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp				
146 355	360	365		
148 caa att aca tta tta aag gcg tca tca agc gaa gtg atg atg ctg cga				1512
149 Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg				
150 370	375	380		
152 gtg gcg cga cgg tac gac gcg gcg acg gac agc gtg ctg ttc gcg aac				1560
153 Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn				
154 385	390	395	400	
156 aac cag gcg tac acg cgc gac aac tac cgc aag gcg ggc atg tcc tac				1608
157 Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr				
158 405	410	415		
160 gtc atc gag gac ctg ctg cac ttc tgt cgg tgt atg tac tcc atg agc				1656
161 Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser				
162 420	425	430		
164 atg gac aat gtg cac tac gcg ctg ctc acc gcc atc gtt ata ttc tca				1704
165 Met Asp Asn Val His Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser				
166 435	440	445		
168 gac cgg cca ggc ctc gag caa ccc ctt tta gtg gag gaa atc cag aga				1752
169 Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg				
170 450	455	460		
172 tac tac ttg aag acg ctg cgg gtt tac att tta aat cag cac agc gcg				1800
173 Tyr Tyr Leu Lys Thr Leu Arg Val Tyr Ile Leu Asn Gln His Ser Ala				
174 465	470	475	480	
176 tcg cct cgc tgc gcc gtg ctg ttc ggc aag atc ctc ggc gtg ctg acg				1848
177 Ser Pro Arg Cys Ala Val Leu Phe Gly Lys Ile Leu Gly Val Leu Thr				
178 485	490	495		
180 gaa ctg cgc acg ctc ggc acg cag aac tcc aac atg tgc atc tcg ctg				1896
181 Glu Leu Arg Thr Leu Gly Thr Gln Asn Ser Asn Met Cys Ile Ser Leu				
182 500	505	510		
184 aag ctg aag aac agg aaa ctt ccg cca ttc ctc gag gag atc tgg gac				1944
185 Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp				
186 515	520	525		
188 gtg gcc gaa gtg tcg acg acg cag ccg acg ccg ggg gtg gcg gcg cag				1992
189 Val Ala Glu Val Ser Thr Thr Gln Pro Thr Pro Gly Val Ala Ala Gln				
190 530	535	540		

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193 Val Thr Pro Ile Val Val Asp Asn Pro Ala Ala Leu
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198 gcggcctgcg ctgagtgcgg gaccgcgcgc gaggagagaa cgctcataga ctggctagtt 2161
200 ttagtggaagt gcacggacgc gatcgtggga ccgcacgcgc gcgtccgtga ggacagtgca 2221
202 aatattaccg ctagggccgg ttcgtacgtg tccggtgacc gacgacgatg atgcgcgtga 2281
204 gattagtga tatatgtgtt gttgaacgtt tggagagtat atttagtgtt gatcgtcggg 2341
206 agcgcgcggc cggcgcgtgt cggcgagctg tccgcgcgc gcgcgcgcgc gcgactccgc 2401
208 gtttttttcg tttgcgaccg gaaaccgagt cggtaactcg gatacgcccg tatgataaga 2461
210 cttcttttcg taaataagtt cacctgtatt gcgcgtacat acgagaatta taaagaaaaa 2521
212 aagtaataata tgaagagatg tttctattgg gtgaaaagtt taaacttatg tttatttacc 2581
214 aaaattaact atacgttgat cgaccttttg actataatat tgtgctgggt cgttggcagc 2641
216 ggccgacgaa cgcgcgccga ccatatttgt ttatataatag tttatgtgag acgttatcgt 2701
218 gtcgtgtcca cttagtcccg attcatgttc caccaggtcg gtgtagtgat cagggcgggc 2761
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222 ttgggagacg ttattcctc 2840
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237 20 25 30
240 Ala Ala Met Val Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr Gly
241 35 40 45
244 Gly Leu Glu Leu Trp Ser Tyr Asp Glu Thr Met Thr Asn Tyr Pro Ala
245 50 55 60
248 Gln Ser Leu Leu Gly Ala Cys Asn Ala Pro Gln Gln Gln Gln Gln
249 65 70 75 80
252 Gln Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro
253 85 90 95
256 Met Pro Pro Thr Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly
257 100 105 110
260 Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp
261 115 120 125
264 Gly Glu Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu
265 130 135 140
268 Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn
269 145 150 155 160
272 Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr
273 165 170 175
276 Lys Asn Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp
277 180 185 190
280 Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu
281 195 200 205
284 Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Ser Thr Cys Lys

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285      210      215      220
288 Asn Lys Arg Arg Glu Lys Glu Ala Gln Arg Glu Lys Asp Lys Leu Pro
289 225      230      235      240
292 Val Ser Thr Thr Thr Val Asp Asp His Met Pro Ala Ile Met Gln Cys
293      245      250      255
296 Asp Pro Pro Pro Pro Glu Ala Ala Arg Ile His Glu Val Val Pro Arg
297      260      265      270
300 Phe Leu Thr Glu Lys Leu Met Glu Gln Asn Arg Leu Lys Asn Val Thr
301      275      280      285
304 Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr
305      290      295      300
308 Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val Thr
309 305      310      315      320
312 Gln Thr Trp Gln Leu Glu Glu Glu Glu Glu Glu Thr Asp Met Pro
313      325      330      335
316 Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val
317      340      345      350
320 Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp
321      355      360      365
324 Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg
325      370      375      380
328 Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn
329 385      390      395      400
332 Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr
333      405      410      415
336 Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser
337      420      425      430
340 Met Asp Asn Val His Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser
341      435      440      445
344 Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg
345      450      455      460
348 Tyr Tyr Leu Lys Thr Leu Arg Val Tyr Ile Leu Asn Gln His Ser Ala
349 465      470      475      480
352 Ser Pro Arg Cys Ala Val Leu Phe Gly Lys Ile Leu Gly Val Leu Thr
353      485      490      495
356 Glu Leu Arg Thr Leu Gly Thr Gln Asn Ser Asn Met Cys Ile Ser Leu
357      500      505      510
360 Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp
361      515      520      525
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369 545      550      555
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377 <220> FEATURE:
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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
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